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#6



OIPF

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/067,956

DATE: 07/24/2002 P.6

TIME: 12:28:55

Input Set : A:\-29-1.app

Output Set: N:\CRF3\07242002\J067956.raw

3 <110> APPLICANT: Barber, Jack
4 Welch, Peter
5 Li, Xinqiang
6 Tritz, Richard
7 Immusol Incorporated
9 <120> TITLE OF INVENTION: Substantially Complete Ribozyme Libraries
11 <130> FILE REFERENCE: 016556-002910US
13 <140> CURRENT APPLICATION NUMBER: US 10/067,956
C--> 14 <141> CURRENT FILING DATE: 2002-07-09
16 <150> PRIOR APPLICATION NUMBER: US 60/093,828
17 <151> PRIOR FILING DATE: 1998-07-22
19 <150> PRIOR APPLICATION NUMBER: US 09/357,741
20 <151> PRIOR FILING DATE: 1999-07-20
22 <160> NUMBER OF SEQ ID NOS: 56
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 12
28 <212> TYPE: RNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence:12 nucleotide
33 tetraloop sequence
35 <400> SEQUENCE: 1
36 ggacuucggu cc 12
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 41
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
45 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR primer P1,
46 3' adeno-associated virus inverted terminal repeat
47 (AAV-ITR) primer
49 <400> SEQUENCE: 2
50 aggaagatct tccattcgcc attcaggctg cgcaactgtt g 41
53 <210> SEQ ID NO: 3
54 <211> LENGTH: 72
55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR primer P2,
60 5' oligonucleotide with sequences for tRNAval
61 promoter and ribozyme library genes
63 <220> FEATURE:

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```

64 <221> NAME/KEY: modified_base
65 <222> LOCATION: (1)..(72)
66 <223> OTHER INFORMATION: n = g, a, c or t
68 <400> SEQUENCE: 3
W--> 69 ataccacaac gtgtgtttct ctggtnnnt tctnnnnnnn ggatcctgtt tccgcccggt 60
70 ttcgaaccgg gg 72
73 <210> SEQ ID NO: 4
74 <211> LENGTH: 72
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR primer P3,
80     oligonucleotide containing ribozyme library gene
81     complementary to P2 oligonucleotide
83 <220> FEATURE:
84 <221> NAME/KEY: modified_base
85 <222> LOCATION: (1)..(72)
86 <223> OTHER INFORMATION: n = g, a, c or t
88 <400> SEQUENCE: 4
W--> 89 ccccggttcg aaaccgggcg gaaacaggat cennnnnnna gaannnnacc agagaaacac 60
90 acgttgttgt at 72
93 <210> SEQ ID NO: 5
94 <211> LENGTH: 40
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR primer P1,
100     5' adeno-associated virus inverted terminal repeat
101     (AAV-ITR) primer
103 <400> SEQUENCE: 5
104 aggagatctg cggaagagcg cccaatacgc aaaccgcctc 40
107 <210> SEQ ID NO: 6
108 <211> LENGTH: 63
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Description of Artificial Sequence:ligation
114     oligonucleotide Oligo 1
116 <220> FEATURE:
117 <221> NAME/KEY: modified_base
118 <222> LOCATION: (1)
119 <223> OTHER INFORMATION: n = phosphorylated g
121 <220> FEATURE:
122 <221> NAME/KEY: modified_base
123 <222> LOCATION: (2)..(63)
124 <223> OTHER INFORMATION: n = g, a, c or t
126 <400> SEQUENCE: 6
W--> 127 natccacccc cennnnnnna gaannnnacc agagaaacac acgttgttgt atattacctg 60
128 gta 63

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RAW SEQUENCE LISTING

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Input Set : A:\-29-1.app

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```

131 <210> SEQ ID NO: 7
132 <211> LENGTH: 18
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <223> OTHER INFORMATION: Description of Artificial Sequence:ligation
138     oligonucleotide Oligo 3
140 <220> FEATURE:
141 <221> NAME/KEY: modified_base
142 <222> LOCATION: (1)
143 <223> OTHER INFORMATION: n = phosphorylated c
145 <400> SEQUENCE: 7
W--> 146 ngggtaccag gtaatata                                18
149 <210> SEQ ID NO: 8
150 <211> LENGTH: 101
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Description of Artificial Sequence:ligation
156     oligonucleotide Oligo 4
158 <220> FEATURE:
159 <221> NAME/KEY: modified_base
160 <222> LOCATION: (1)
161 <223> OTHER INFORMATION: n = phosphorylated a
163 <220> FEATURE:
164 <221> NAME/KEY: modified_base
165 <222> LOCATION: (2)..(101)
166 <223> OTHER INFORMATION: n = g, a, c or t
168 <400> SEQUENCE: 8
W--> 169 nattctgcag atatccatca cactggcgagg gatcctcgag nnnnnnnnag aannnnacca 60
170 gagaaacaca cggacttcgg tccgtggtat attacctggt a          101
173 <210> SEQ ID NO: 9
174 <211> LENGTH: 36
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: Description of Artificial Sequence:ligation
180     oligonucleotide Oligo 5
182 <220> FEATURE:
183 <221> NAME/KEY: modified_base
184 <222> LOCATION: (1)
185 <223> OTHER INFORMATION: n = phosphorylated c
187 <400> SEQUENCE: 9
W--> 188 ntcgaggatc cccgccagtg tgatggatat ctgcag            36
191 <210> SEQ ID NO: 10
192 <211> LENGTH: 48
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:

```

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Input Set : A:\-29-1.app

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```

197 <223> OTHER INFORMATION: Description of Artificial Sequence:ligation
198     oligonucleotide Oligo 6
200 <220> FEATURE:
201 <221> NAME/KEY: modified_base
202 <222> LOCATION: (1)
203 <223> OTHER INFORMATION: n = phosphorylated g
205 <400> SEQUENCE: 10
W--> 206 ncgtaccagg taatatacca cggaccgaag tccgtgtggt tctctggt          48
209 <210> SEQ ID NO: 11
210 <211> LENGTH: 87
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Description of Artificial Sequence:ligation
216     oligonucleotide Oligo 7
218 <220> FEATURE:
219 <221> NAME/KEY: modified_base
220 <222> LOCATION: (1)
221 <223> OTHER INFORMATION: n = phosphorylated c
223 <220> FEATURE:
224 <221> NAME/KEY: modified_base
225 <222> LOCATION: (2)..(87)
226 <223> OTHER INFORMATION: n = g, a, c or t
228 <400> SEQUENCE: 11
W--> 229 ngaaaccggg cggaacagg atccnnnnnn nnagaannnn accagagaga aacacacgga 60
230 cttcggtccg tggatatatta cctggta          87
233 <210> SEQ ID NO: 12
234 <211> LENGTH: 22
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Description of Artificial Sequence:ligation
240     oligonucleotide Oligo 8
242 <220> FEATURE:
243 <221> NAME/KEY: modified_base
244 <222> LOCATION: (1)
245 <223> OTHER INFORMATION: n = phosphorylated g
247 <400> SEQUENCE: 12
W--> 248 ngatcctggt tccgcccggt tt          22
251 <210> SEQ ID NO: 13
252 <211> LENGTH: 48
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Description of Artificial Sequence:ligation
258     oligonucleotide oligo 3
260 <220> FEATURE:
261 <221> NAME/KEY: modified_base
262 <222> LOCATION: (1)

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RAW SEQUENCE LISTING

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Input Set : A:\-29-1.app

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```

263 <223> OTHER INFORMATION: n = phosphorylated c
265 <400> SEQUENCE: 13
W--> 266 ngcgtaggac gtaatatatacc acggaccgaa gtccgtgtgt ttctctgg 48
269 <210> SEQ ID NO: 14
270 <211> LENGTH: 92
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Description of Artificial Sequence:libbam PCR
276 primer
278 <220> FEATURE:
279 <221> NAME/KEY: modified_base
280 <222> LOCATION: (1)..(92)
281 <223> OTHER INFORMATION: n = g, a, c or t
283 <400> SEQUENCE: 14
W--> 284 ccccggtggg atccnnnnnn nnagaavnnn accagagaaa cacacggact tcgggtccgtg 60
285 gtatattacc tggtagcggt ttttgcat tt 92
288 <210> SEQ ID NO: 15
289 <211> LENGTH: 27
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Description of Artificial Sequence:EBVlibeco PCR
295 primer
297 <400> SEQUENCE: 15
298 tggggtggga gatatacgctg ttcctta 27
301 <210> SEQ ID NO: 16
302 <211> LENGTH: 87
303 <212> TYPE: DNA
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: Description of Artificial Sequence:annealing
308 oligonucleotide Oligol (underline)
310 <220> FEATURE:
311 <221> NAME/KEY: modified_base
312 <222> LOCATION: (1)
313 <223> OTHER INFORMATION: n = phosphorylated c
315 <220> FEATURE:
316 <221> NAME/KEY: modified_base
317 <222> LOCATION: (2)..(87)
318 <223> OTHER INFORMATION: n = g, a, c or t
320 <400> SEQUENCE: 16
W--> 321 ngcgtaggac gtaatatatacc acggaccgaa gtccgtgtgt ttctctggtn nnnctctnnn 60
W--> 322 nnnnnggata ctgtttccgc cgggtt 87
325 <210> SEQ ID NO: 17
326 <211> LENGTH: 22
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/067,956

DATE: 07/24/2002
TIME: 12:28:56

Input Set : A:\-29-1.app
Output Set: N:\CRF3\07242002\J067956.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 26,27,28,29,34,35,36,37,38,39,40
Seq#:4; N Pos. 33,34,35,36,37,38,39,44,45,46,47
Seq#:6; N Pos. 1,13,14,15,16,17,18,19,24,25,26,27
Seq#:7; N Pos. 1
Seq#:8; N Pos. 1,41,42,43,44,45,46,47,48,53,54,55,56
Seq#:9; N Pos. 1
Seq#:10; N Pos. 1
Seq#:11; N Pos. 1,25,26,27,28,29,30,31,32,37,38,39,40
Seq#:12; N Pos. 1
Seq#:13; N Pos. 1
Seq#:14; N Pos. 15,16,17,18,19,20,21,22,28,29,30
Seq#:16; N Pos. 1,50,51,52,53,58,59,60,61,62,63,64,65
Seq#:17; N Pos. 1
Seq#:18; N Pos. 1
Seq#:20; N Pos. 5
Seq#:21; N Pos. 12
Seq#:22; N Pos. 56
Seq#:25; N Pos. 5
Seq#:28; N Pos. 5
Seq#:30; N Pos. 5,6,7,8
Seq#:36; N Pos. 1,39
Seq#:37; N Pos. 12
Seq#:40; N Pos. 25,26,30,31,35,36,38
Seq#:42; N Pos. 1,2,3,4,5,6,7,8,9,10,15,16,17,18
Seq#:43; N Pos. 5,16,17,18,19
Seq#:44; N Pos. 4,5,9,10,14,15
Seq#:45; N Pos. 1,2,3,8,9,10,11
Seq#:46; N Pos. 8,9,11
Seq#:47; N Pos. 1,2,3,4,5,6,7,13,14,15
Seq#:48; N Pos. 1,2,3,5,9,10,11,12,13,14,15
Seq#:49; N Pos. 8,9,11,15,16,17,18,19,20,21
Seq#:50; N Pos. 1,2,3,4,5,6,7,8,13,14,15,16
Seq#:51; N Pos. 1,2,3,4,9,10,11,12,13,14,15,16
Seq#:52; N Pos. 1,2,3,4,9,10,11,12,13,14,15,16

VARIABLE LOCATION SUMMARY

DATE: 07/24/2002

PATENT APPLICATION: US/10/067,956

TIME: 12:28:56

Input Set : A:\-29-1.app

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Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:3; N Pos. 26,27,28,29,34,35,36,37,38,39,40
Seq#:4; N Pos. 33,34,35,36,37,38,39,44,45,46,47
Seq#:6; N Pos. 1,13,14,15,16,17,18,19,24,25,26,27
Seq#:7; N Pos. 1
Seq#:8; N Pos. 1,41,42,43,44,45,46,47,48,53,54,55,56
Seq#:9; N Pos. 1
Seq#:10; N Pos. 1
Seq#:11; N Pos. 1,25,26,27,28,29,30,31,32,37,38,39,40
Seq#:12; N Pos. 1
Seq#:13; N Pos. 1
Seq#:14; N Pos. 15,16,17,18,19,20,21,22,28,29,30
Seq#:16; N Pos. 1,50,51,52,53,58,59,60,61,62,63,64,65
Seq#:17; N Pos. 1
Seq#:18; N Pos. 1
Seq#:20; N Pos. 5
Seq#:21; N Pos. 12
Seq#:22; N Pos. 56
Seq#:25; N Pos. 5
Seq#:28; N Pos. 5
Seq#:30; N Pos. 5,6,7,8
Seq#:36; N Pos. 1,39
Seq#:37; N Pos. 12
Seq#:40; N Pos. 25,26,30,31,35,36,38
Seq#:42; N Pos. 1,2,3,4,5,6,7,8,9,10,15,16,17,18
Seq#:43; N Pos. 5,16,17,18,19
Seq#:44; N Pos. 4,5,9,10,14,15
Seq#:45; N Pos. 1,2,3,8,9,10,11
Seq#:46; N Pos. 8,9,11
Seq#:47; N Pos. 1,2,3,4,5,6,7,13,14,15
Seq#:48; N Pos. 1,2,3,5,9,10,11,12,13,14,15
Seq#:49; N Pos. 8,9,11,15,16,17,18,19,20,21
Seq#:50; N Pos. 1,2,3,4,5,6,7,8,13,14,15,16
Seq#:51; N Pos. 1,2,3,4,9,10,11,12,13,14,15,16
Seq#:52; N Pos. 1,2,3,4,9,10,11,12,13,14,15,16

VERIFICATION SUMMARY

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Input Set : A:\-29-1.app

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:60
L:340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:512 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:512 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0
L:846 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0
L:864 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:877 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:50
L:877 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:50
L:877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:890 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:890 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:890 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:903 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:52
L:903 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:0